	<110>	SUNGKYUNKWAN UNIVERSITY			
	<120>	Composition for treating virus i	nfection disease comprising	Jab1	
5	<160>	6			
	<170>	KopatentIn 1.71			
10	<210> <211> <212> <213>	1 1262 DNA Homo sapiens			
15	<220> <221> <222> <223>	gene (1)(1262) Jab1			
20	<220> <221> <222>	CDS (94)(1095)			
25	<400> ctggtgggg	l ga aggtccaaag cccgcacgct gaggco	ccagt agaagaaagt tgcatcttga	60	
30	ttgtggago	g acagettete eggtgeeteg gee	atg gca gct tcc ggg Met Ala Ala Ser Gly 1 5	108	
30		tg gcc cag aaa acc tgg gaa ttg gc Met Ala Gln Lys Thr Trp Glu Leu 10 15	Ala Asn Asn Met Gln Glu	156	
35		ngt atc gat gaa atc tac aaa tat gad ier lle Asp Glu lle Tyr Lys Tyr A 25 30		204	
40		tg gcg gcg aaa ccc tgg act aag ga eu Ala Ala Lys Pro Trp Thr Lys A 40 45		252	
45		aa atc tca gca ttg gct cta ctg aaa Lys Ile Ser Ala Leu Ala Leu Leu 60		300	
50		ga ggc aac ttg gaa gtg atg ggt ttg Gly Gly Asn Leu Glu Val Met Gly 75		348	

	gac ggc gag acc atg atc atc atg gac agt ttc gct ttg cct gta gag Asp Gly Glu Thr Met Ile Ile Met Asp Ser Phe Ala Leu Pro Val Glu 90 95 100	396
5	ggc aca gaa act cga gta aat gct caa gct gct gcg tat gag tat atg Gly Thr Glu Thr Arg Val Asn Ala Gln Ala Ala Ala Tyr Glu Tyr Met 105 110 115	444
10	gct gca tac ata gaa aat gcc aaa cag gtt ggc cgc ctt gag aat gca Ala Ala Tyr Ile Glu Asn Ala Lys Gln Val Gly Arg Leu Glu Asn Ala 120 125 130	4 92
15	atc ggt tgg tat cat agc cac cct ggt tat ggc tgc tgg ctc tcc ggg lle Gly Trp Tyr His Ser His Pro Gly Tyr Gly Cys Trp Leu Ser Gly 135 140 145	540
20	att gat gtt agt aca cag atg ctg aac cag cag ttt caa gaa cca ttt lle Asp Val Ser Thr Gln Met Leu Asn Gln Gln Phe Gln Glu Pro Phe 150 155 160 165	588
20	gta gca gtg gtg att gat cca acc aga aca atc tct gca gga aaa gtg Val Ala Val Val Ile Asp Pro Thr Arg Thr Ile Ser Ala Gly Lys Val 170 175 180	636
25	Asn Leu Gly Ala Phe Arg Thr Tyr Pro Lys Gly Tyr Lys Pro Pro Asp 185 190 195	684
30	gaa gga cct tct gag tac cag act atc cca ctt aat aaa ata gaa gat Glu Gly Pro Ser Glu Tyr Gln Thr Ile Pro Leu Asn Lys Ile Glu Asp 200 205 210	732
35	ttt ggc gtg cac tgc aaa caa tat tat gcc tta gaa gtc tca tat ttc Phe Gly Val Ḥis Cys Lys Gln Tyr Tyr Ala Leu Glu Val Ser Tyr Phe 215 220 225	780
10	aaa tca tct ttg gat cgt aaa cta ctt gag ctt ttg tgg aat aaa tac Lys Ser Ser Leu Asp Arg Lys Leu Leu Glu Leu Leu Trp Asn Lys Tyr 230 235 240 245	828
10	tgg gtg aat acc ctg agt tcc tct agc ttg ctt act aat gca gac tac Trp Val Asn Thr Leu Ser Ser Ser Leu Leu Thr Asn Ala Asp Tyr 250 255 260	876
45	acc aca ggc cag gtg ttt gat ttg tct gag aag tta gag cag tcg gaa Thr Thr Gly Gln Val Phe Asp Leu Ser Glu Lys Leu Glu Gln Ser Glu 265 270 275	924
50	gcc caa ctg gga cgt ggc agt ttc atg ttg ggc tta gaa aca cat gac Ala Gln Leu Gly Arg Gly Ser Phe Met Leu Gly Leu Glu Thr His Asp	972

280	285	290
-----	-----	-----

5	cgc aag tcg gaa gac aaa ctt gcc aaa gct act aga gac agc tgt aaa Arg Lys Ser Glu Asp Lys Leu Ala Lys Ala Thr Arg Asp Ser Cys Lys 295 300 305	1020
10	acc acc ata gaa gcc atc cat gga ctg atg tct cag gtt att aag gat Thr Thr Ile Glu Ala Ile His Gly Leu Met Ser Gln Val Ile Lys Asp 310 315 320 325	1068
	aaa ctg ttt aat cag att aac gtt gct — tagtt accaccaagt acttctcaaa Lys Leu Phe Asn Gln Ile Asn Val Ala 330	1120
15	gctggtgtgt ggaaggaaaa gaagctcaag taacactttt aacccagtta ccaaaactca	1180
	gattagaaga ctaaggtgct gtgtggtgtc ctgagtatta gcactgtaat aaaactatca	1240
20	cgtgaaaaaa aaaaaaaaaa aa	1262
	<210> 2 <211> 334	
25	<212> PRT <213> Homo sapiens	
30	<400> 2 Met Ala Ala Ser Gly Ser Gly Met Ala Gln Lys Thr Trp Glu Leu Ala 1 5 10 15	
	Asn Asn Met Gln Glu Ala Gln Ser Ile Asp Glu Ile Tyr Lys Tyr Asp 20 25 30	
35	Lys Lys Gln Gln Gln Glu Ile Leu Ala Ala Lys Pro Trp Thr Lys Asp 35 40 45	
	His His Tyr Phe Lys Tyr Cys Lys Ile Ser Ala Leu Ala Leu Leu Lys 50 55 60	
40	Met Val Met His Ala Arg Ser Gly Gly Asn Leu Glu Val Met Gly Leu 65 70 75 80	
45	Met Leu Gly Lys Val Asp Gly Glu Thr Met Ile Ile Met Asp Ser Phe 85 90 95	
	Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ala Ala 100 105 110	
50	Ala Tyr Glu Tyr Met Ala Ala Tyr Ile Glu Asn Ala Lys Gln Val Gly 115 120 125	

	Arg Leu 130	Glu Asn Ala	lle Gly Ti 135	rp Tyr	His Ser I	His Pro Gl	y Tyr Gly	r
5	Cys Trp 145	Leu Ser Gly	Ile Asp V 150	'al Ser	Thr Gln 1			ln 160
10	Phe Gln	Glu Pro Phe 165	Val Ala V	'al Val	Ile Asp P 170	ro Thr Ar	g Thr Ile 175	
10	Ser Ala (Gly Lys Val <i>I</i> 180	Asn Leu C	Gly Ala 189		Thr Tyr F	Pro Lys G 190	ly
15		Pro Pro Asp 195		Pro Ser 200	Glu Tyr	Gln Thr II 205	e Pro Le	Li
	Asn Lys 210	lle Glu Asp I	Phe Gly V 215	al His	Cys Lys	Gln Tyr T 220	yr Ala Le	u
20	Glu Val S 225	Ser Tyr Phe	Lys Ser S 230	Ser Leu	Asp Arg 23			eu 240
25	Leu Trp	Asn Lys Tyr 245	Trp Val	Asn Th	ır Leu Se 250	er Ser Ser	Ser Leu 1 255	Leu
	Thr Asn	Ala Asp Tyr 260	Thr Thr	Gly Gli 26			Ser Glu I 270	∠ys
30		Gln Ser Glu 275		eu Gly 280	Arg Gly :	Ser Phe M 285	et Leu Gl	ι y
	Leu Glu 290	Thr His Asp	Arg Lys 3 295	Ser Glu	ı Asp Lys	s Leu Ala l 300	Lys Ala T	`hr
35	Arg Asp 305	Ser Cys Lys	Thr Thr 310	Ile Glu	Ala Ile F 31			r 320
40	Gln Val I	le Lys Asp L 325	ys Leu P	he Asn	Gln Ile A	Asn Val Al	a	
	<210> <211>	3 32						
45	<212> <213>	DNA Artificial S	equence					
	<220> <223>	primer for	WNV-Cp	amplif	ication			

	<400>	3	
	ccggaat	tct ctaaaaaacc aggtggcccc gg	32
5	<210>	4	
	<211>	33	
	<212>	DNA	
	<213>	Artificial Sequence	
10	<220>		
	<223>	primer for WNV-Cp amplification	
	<400>	4	
15	gactage	ggt cgcacccgcg catcgagctc gcc	33
	<210>	5	
	<211>	32	
20	<212>	DNA	
	<213>	Artificial Sequence	
	<220>		
25	<223>	primer for DNA sequencing	
	4400>	_	
	<400>	5	0.0
	ctattega	tg atgaagatac cccaccaaac cc	32
30			
	<210>	6	
	<211>	33	
	<212>	DNA	
35	<213>	Artificial Sequence	
	<220>		
	<223>	primer for DNA sequencing	
40	<400>	6	
		at gactttttgg ggcgttcaag tga	33
	_	= 00000	~ ~ ~

.....